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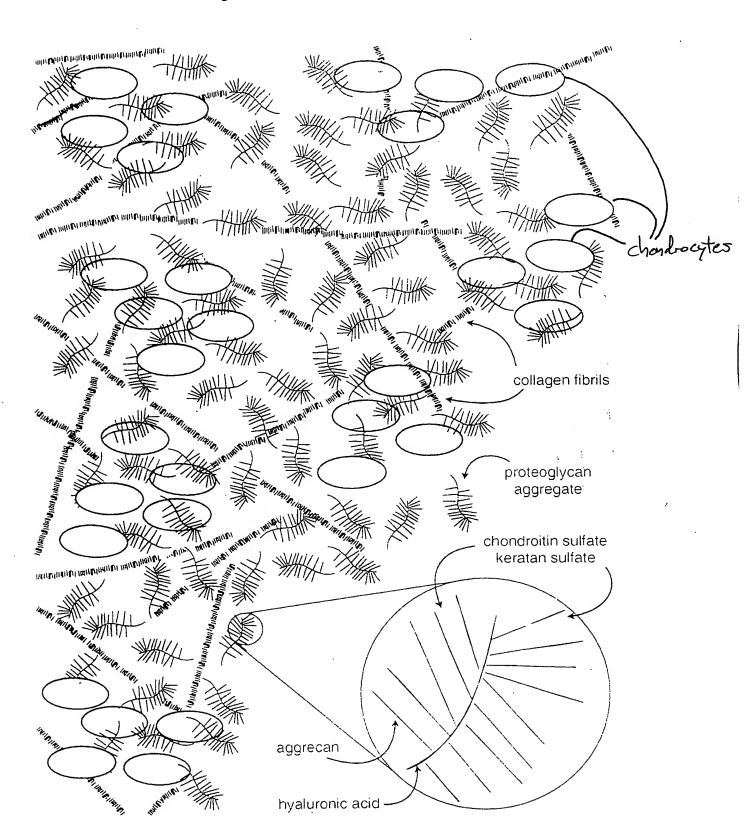
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Figure 1 - Healthy Nucleus Pulposus Tissue



Cross-linked Mainix KIRULE ZO

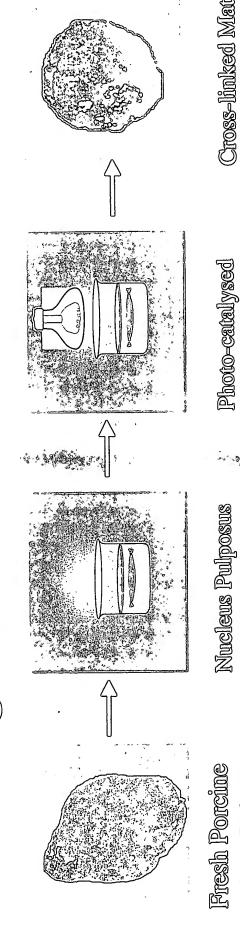
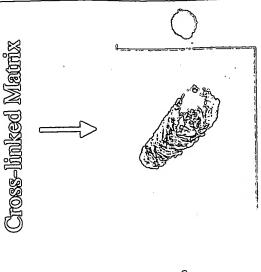


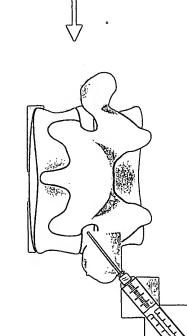
Photo-catallysed cross-linking

in HISHIS

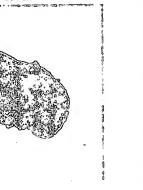
Nucleus Pulposus



Sterille, Lyophillized Cross-linked Matrix



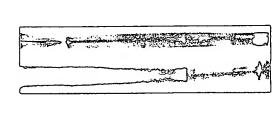
Administer in 22G Syringe



Rehydrated Matrix or

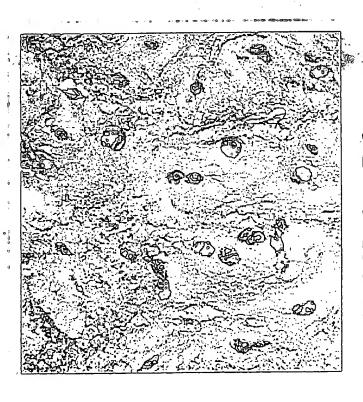
Matrix/BIP/serum

E BINGILL S

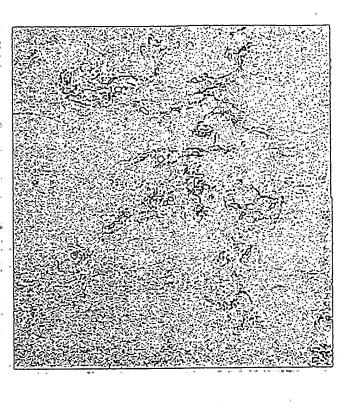


oLame A.: Non cross-linked control shows substantial protein extraction ollane B: Cross-linked matrix démonstrates reduced protein extraction

Nucleus Pulposuis versus Cross-linked Matrix Rigure 4. Comparison of Kresh Porcine



o intact pericellular matrix "nests" o round, nucleated chondrocytes Presh Nucleus Pulposus



Cross-linked Matrix

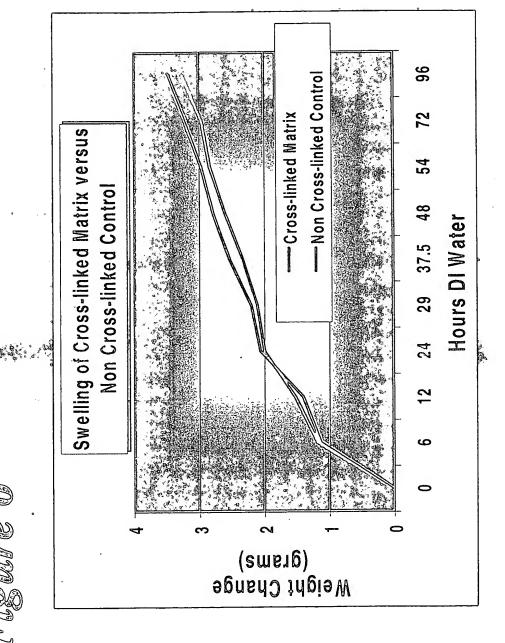
- o dismipted, cremated cell fragments
- o minimal cell membrane material or further isopropanol sterilization

Kigure S



∭ ₩

oLame B: Pepsin digests of cross-linked matrix does not react with Type II collagen antibodie olane A: Pepsin digests of non cross-linked control react with Type II collagen antibodies



ross-linked matrix retains 95% hydraulic capacit

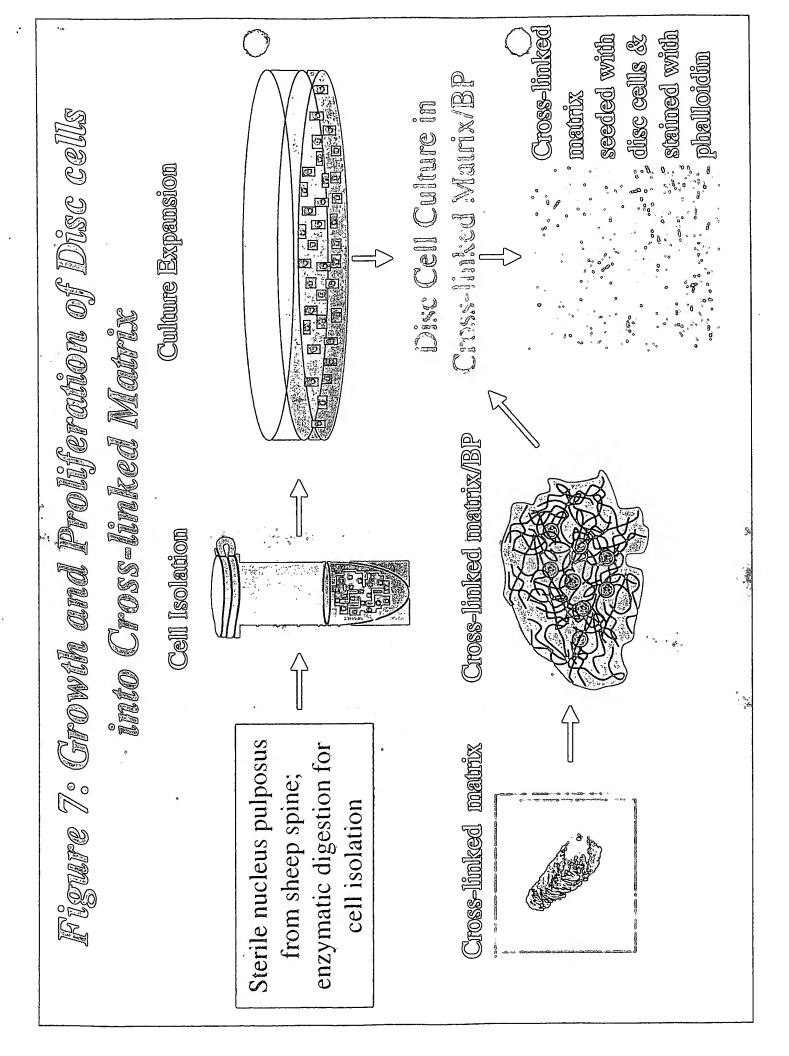
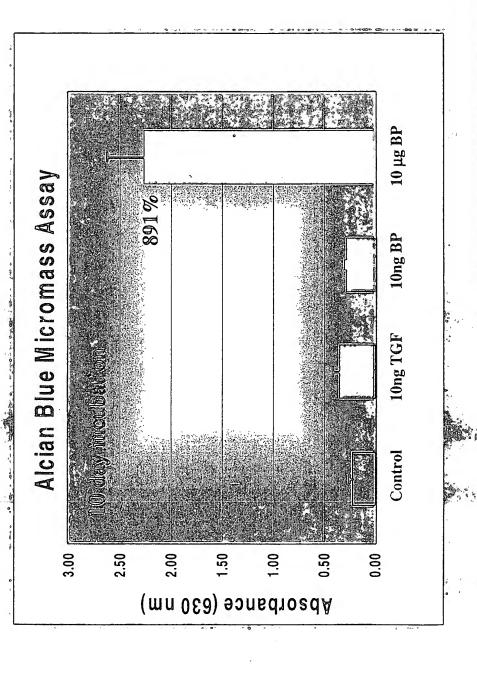
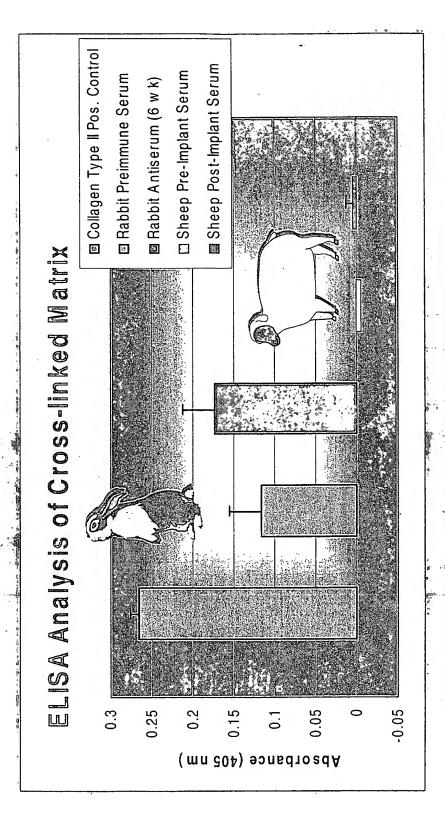


Figure 8: Growth Factor Stimulation of Matrix Synthesis

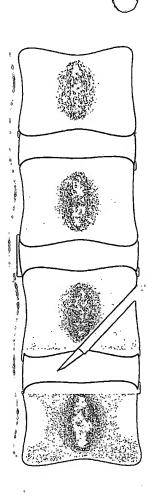


o Signifficant stimulation of mithix production only at ug BIP concentrations



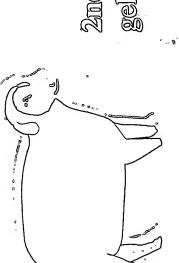
o Low antilbody titers to cross-linked matrix in rabbit immunizations o No serum antilbodies to cross-linked matrix in vivo (1st sheep)

1st operation: annulus stabs to create two degenerative discs

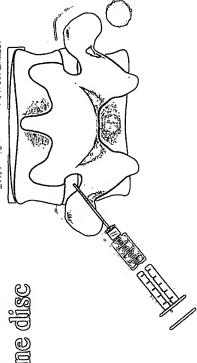


Wait 2 months

2nd operation: Cross-linked matrix/BP gel treatment injection to one disc



- Histomorphometry
- o MIRI/radiographs
- Immume response



Sacriffice: 2, 4, and 6 months

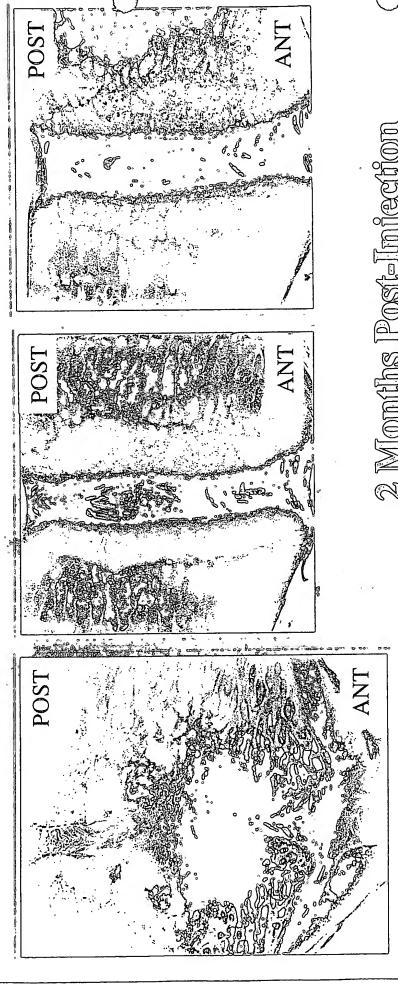
Figure II: Radiograph-Pilot Study #1 2 Months Post Ingection (Cross-linked matrix/BP)



o Treated and Control discs: notinal size and appearance of disc structures

o Untreated disc. disjunct endinates, bone resorption and remodelling

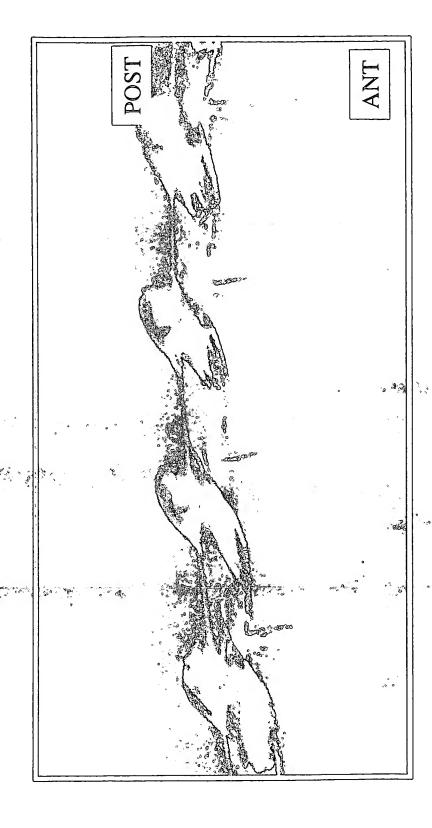
Figure 12: Histology- Pilot Study #1



2 Months Post-Injection

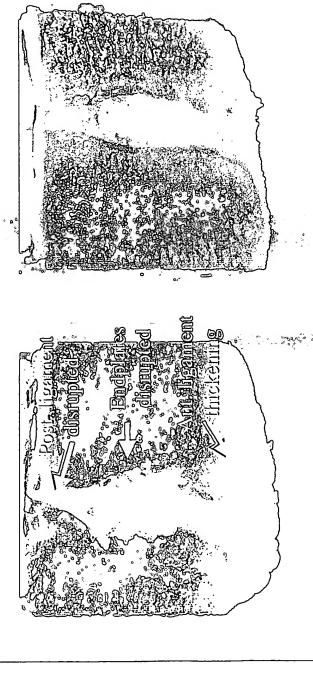
- o Unitreated disc exhilbits extensive degeneration
- o Cross-linked matrix/BP-treated disc retains mormal structures similar to Control disc

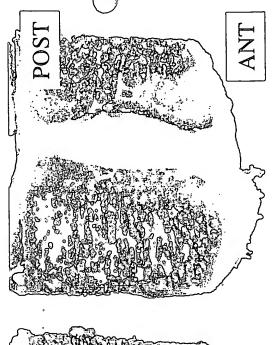
Figure 13: Radiograph-Pilot Study #1 4 Months Post Injection (Cross-linked matrix/BP)



o No apparent radiographic differences between discs in 4 month sheep.

Figure 14: Histology- Pilot Study #1

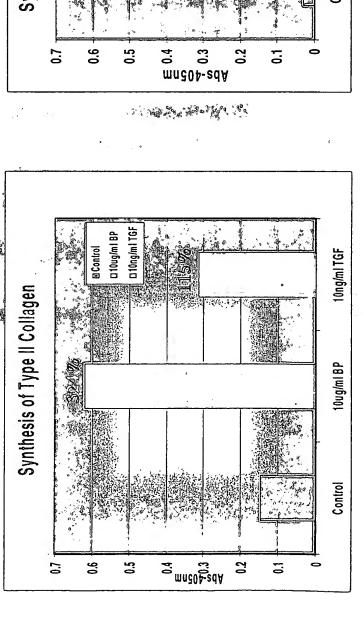


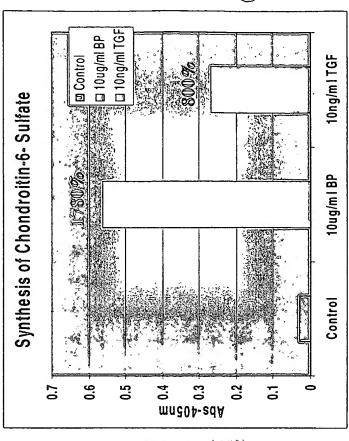


4. Months Post-Injection

- o Unitreated disc exhilbits degenerative changes
- o Cross-linked matrix/BP-treated disc similar to control disc. normal gelatinous pucleus, regular annulus, intact endiplates

Iype II Collagen & Chondroitin-6-Sulfate Synthesis Figure 15: Crowth Factor Stinulation of

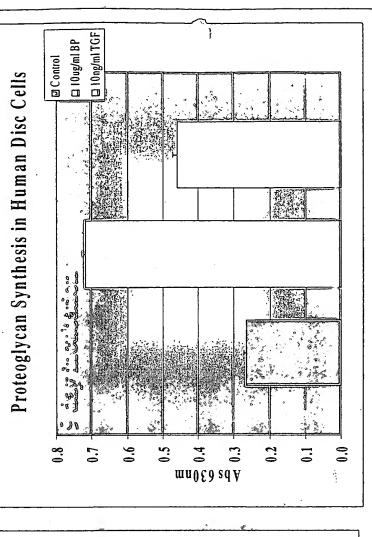


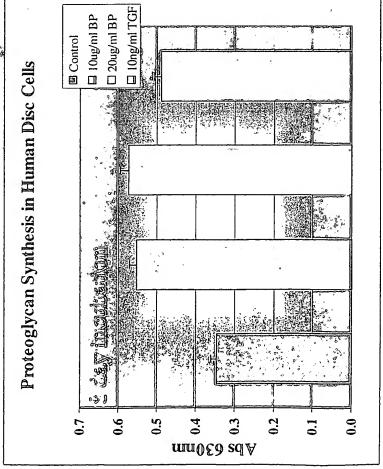


Synthesis in Human Intervertebral Disc Nucleus Pulposus Cells Figure 16: Growth Factor Stimulation of Proteoglycan

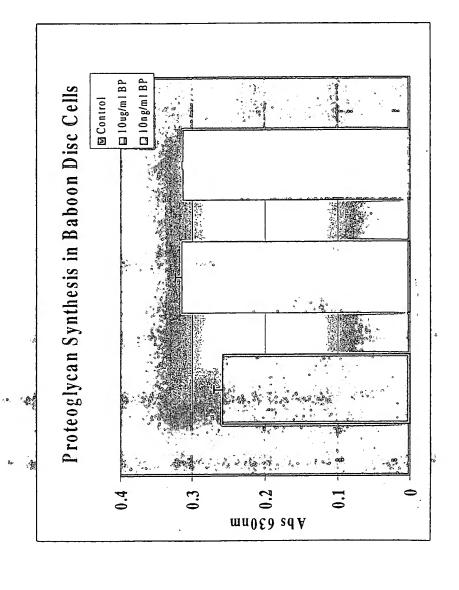
Figure 16a







Profeoglycan Synthesis in Baboon Infervertebral Disc Nacleus Pulposus Cells Figure II: Growth Factor Stimulation of



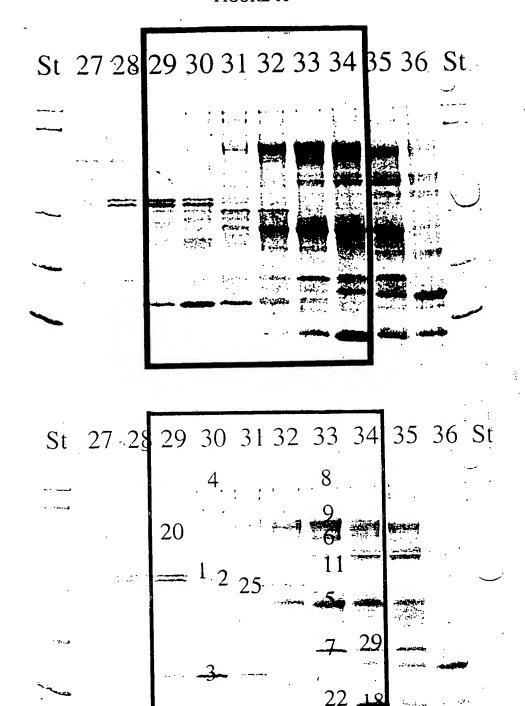


FIGURE 19

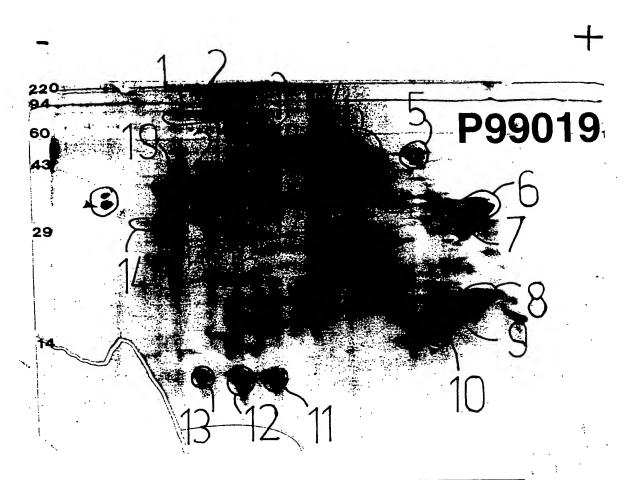
St BP 4/8

Band No.	Identity
1	histone H1 c
2	histone H1.c
3	ribosomal protein RS20
4	similar to ribosomal protein LORP
5	BMP-3
6	α2 macroglobulin RAP & BMP-3
7	similar to ribosomal protein LORP
8	BMP-3
9	BMP-3
11	ribosomal protein RL6 & BMP-3
18	TGF-β2/SPP24
20	Factor H
22	TGF-β2
25	BMP-3 & H1.x
29	BMP-3 & ribosomal protein RL32

FIGURE 20

P99019

FIGURE 21



No.	Identity	No.	Identity
l	Factor XIII	11	TGF- β2/SPP24
2	LORP	12	SPP24
3	LORP	12	TGF- β2/SPP24
4		14	lysyl oxidase
5	RL3	15	lysyl oxidase
6		16	lysyl oxidase
7		17	lysyl oxidase
8		18	BMP-3
9		19	cathepsin L
10		20	
		21	RS3a

FIGURE 22

Corected: 1077/199 2:30 PU Sumply: 22 Culexe 1012/89 3-21 Ft. Sample, 75 PSO March Histor Tumbliko Selegasi; 15 1 OFF Neglavo lara OFF Timed ion Selector, 16.1 OFF Negative lons: OFF Notice Ratio 1483 Vinus Par.a. 1,057 Columbia University /HEIMI Protein Core PSD Miner Pass Columbia University /HHMI Protein Core Figure 23 B (Band 2) Stars Assinged 255 Programs 9 Casult Low Masa Gate: 529 0 W.K. Yang Find Pressure 1584-Low Mass Gale: XOD Law 1565 1385 : 1024. Scarts Average 1: 236 Ofgnal Fixnare: c/wspatricesbynap10995umerbame(Q7.ms Pw Fire # 1 CWUYAGERDATANWGIR999ARNESSI/200PMIS Organi Flent, e. c'unyageddalahnag 1053dqesfo wetO. ms Fris Fie e i ; c'utyageEnDaTabbagitgeGGESTISHXOFH MS 7531 23. Cord Volume St. CCC N Gard Volkage: B4.000 % Surde Vive Voltage: 0.075 % Acce Milling Volumes. NAVY Apprehimatory Volume LLCCO . 141. Somment BARNES-2, trypeln, 7.5 % :£37 æ3 ommerd: barnes-4, Lys 5% 3 METERS LDETERM ANTON LDEIDYA 200 . 1 ģ 2 Colected 1G12092:13 PM Serget 74 3533, 46 Sampte. 76 PSD Metar Reto

Trans ton Belletin 18.1 OF F

Negative form COF Savisky Culay Childre + 7 Ponts = 19 Savesky. Colay Order = 2 Points = 19 Limor Rains 1 Old Martin Rates LIGHT Columbia University /HHMI Protein Core PS-D former Rates Calculad: VO12/5/2 2 31 FM Columbia University /IHIMI Protein Core Scars Averaged 236 Pressure: 1700-05 Flqure 23 A. (Band 1) Low Mass Gide; \$400 Scars Averaged 155 THE FIRE I CONDYAGENDATAMAGIUMDIGESTSMOOTHMS Cryna Parane c'voracettatmas (SSM) partamadè ma Inchèse e c'voracettatantant (SSM) de contra de (4,ta) e (47, 23.03.52 Curior Vive Vortages 9 075 % October Vive Vortages 9 075 % October 50 001 Date: Sti CN Accelerant Votage, 2010 mentratory transportation £.c 5 (5) omment BARNES-1, hypsin, 7.5 % Comment BARNES-3, Lypsin, 7.5 % 12,57433 1137 11 Busines UPERSON Method, LOE 10034 Mode Least Mode Linear , a 12.0 1077 ż ş, . C3 XX 3

Figure 23 D (Band 4

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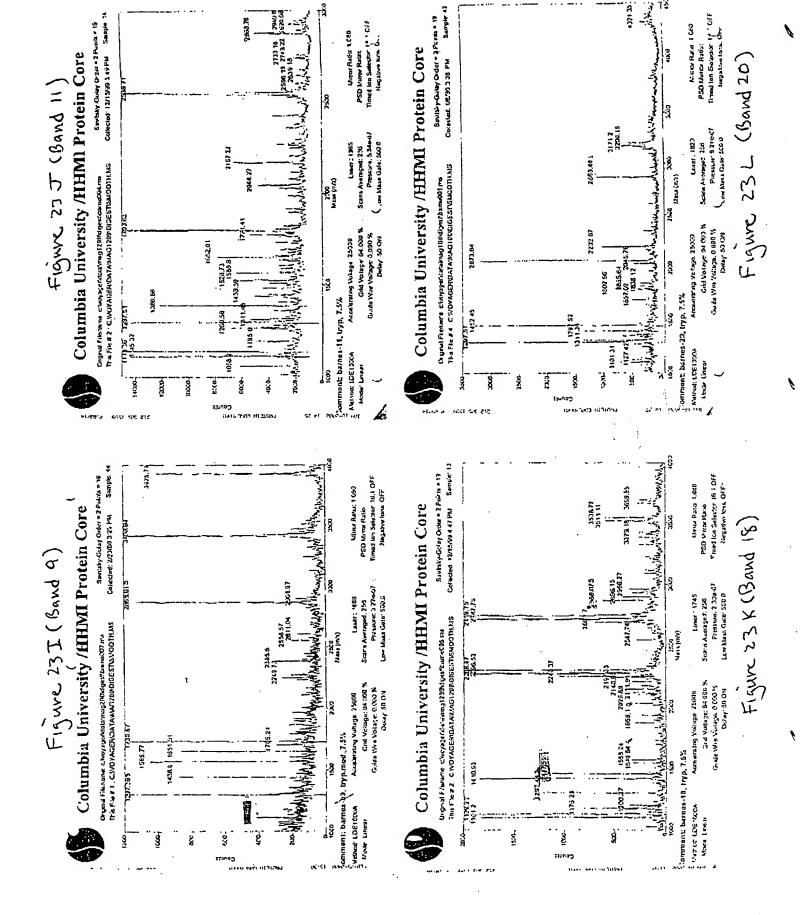
Kai

Figure 23C (Band 3)

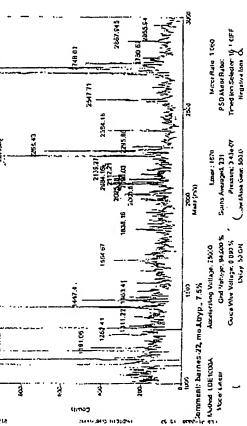
Fored ton Sobetter 16 1 OFF Colociad, 11/1031 3; IB PM Sample E4 impeten Sobodor 16 i Ciff Nogarine tons: Off Santaky-Gury Order = 2 Ports = 19 Name Rada, 1.850 Many Ratio, 1 (M) PSD Kunei Rauo 7668.1 344. Columbia University AIHMI Protein Core Culected, Ibs.29 1-14 PM Columbia University /HHMI Protein Core Flyure 23H (Band 8) Figure 23 F (Band 6) Scens Averaged 256 Pressure 4 014017 Low Mass Galar 568 3 766145 Pressure: 4.030-07 Laser 1865 Scan Averaged, 245 Linker . 1895 Odgraf Filmania e Voyog eMalaineg 11530 geanson (MS. ma Fri Fila # 1 Evioox GER CATAUAG 11990 MGE BYSVOOTH MS Onginal Fibrains choyagendaining 18996; esthannoù lina Fins Fia a i Civoyagendatavaksisechisestisivoothais (מידן מערון (2.m) ese (11.7x) Guca Vatage 94.000 % Study Authority 1015 % Ducks Wile Vellage: 4 015 % Gra Votage: 94.603 % Guide With Vollage: 0.075 % Deby: 40 ON Accelerating Visions 20043 Acceerating Vorzew 2500) 1631.69 omment barnes-3, Lryp, 7.5% Formment: barnes tryps F6 155 33 Method LCE 1032A 250011 COS PREPARITEE I STORY Ş 3 9 ġ ea an d (65) many die Collected, 17/10/59 J. 11 PM Survet 65 PEO Jance Haba 1780 PEO Jance Haba Trand len Soviciar II * CPF Tungalna lens: Co. 1875.HF Sample, 35 Samaky Gody Order a 2 Portal # 19 Throad han Selector 15 t OFF Hepsture Lives OTF Maria Ratio 1,063 12/12/51 **550 838** See SIA Columbia University /HHMI Protein Core PSD Name Rador emř.3 Columbia University /HHMII Protein Core Marie Land Company and Company of the Company of the Company Colocied, 10/5/23 1 15 PM Figure 23 E (Band 5) Figure 236 (Band 7 Scans Averaged 256
Pressure 1,66e-07
Com Mess Coty (CO) 2858. N STD. Scans Averaged: 121

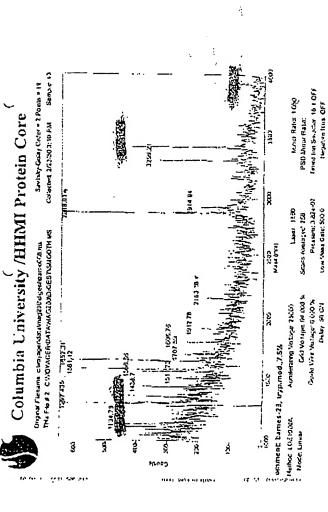
Pressure; 3-65e-07

Low Nass Gan 3000 Luc. 1955 60%1 : racau) Org. ral Flarame: civayayanJandalamay 1994/gradkanow_Orb.ma This Fire 6.1 * CIVIDYAGERGANJAWAGI189DQGESTISSHOOTH MS Ongraf Flanama. Ethograpordalownag (GROKEGERCharmM) 2716 Tyn Fre e 1 i C WDYAGERCOATAWAG (GROKEKERTSINGOTH MS 2610 Mises (red) 1752.62 Gred Vorsige" S4 CGG % Gusta Wite Vollage 0.275 % Grivaters of COO"6 Accelerating Votage 2000 Curie What Working in 1975 's. Anzelo arrej Volasje: 7000 Conment: Samee-7, tryp, 7.5% T.37.33 975 omment: barnes tryps #5 1033,3 Antica. LDE 1000A 111332 Arabad LDEICKA Vede Links Š 33.0



Columbia University /HKIMI Protein Core Occupillaneae chargestating confession (Sand 22) The first Three chargestating confession (Sand Core South Columbia University /HKIMI Protein Core South Columbia Chargestating Columbia (Sand Core South Columbia Chargestating Columbia (Sand Core South Columbia (Sand Columbia) South Columbia South Colum





Frywe 23 O (Band 29)

Figure 23 N (Band 25)

Columbia University /HHMI Protein Core

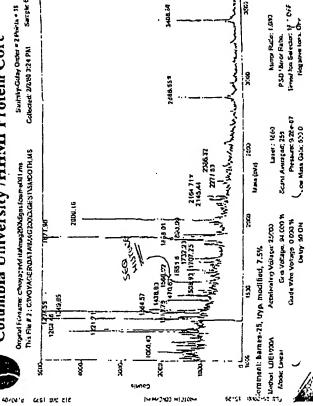
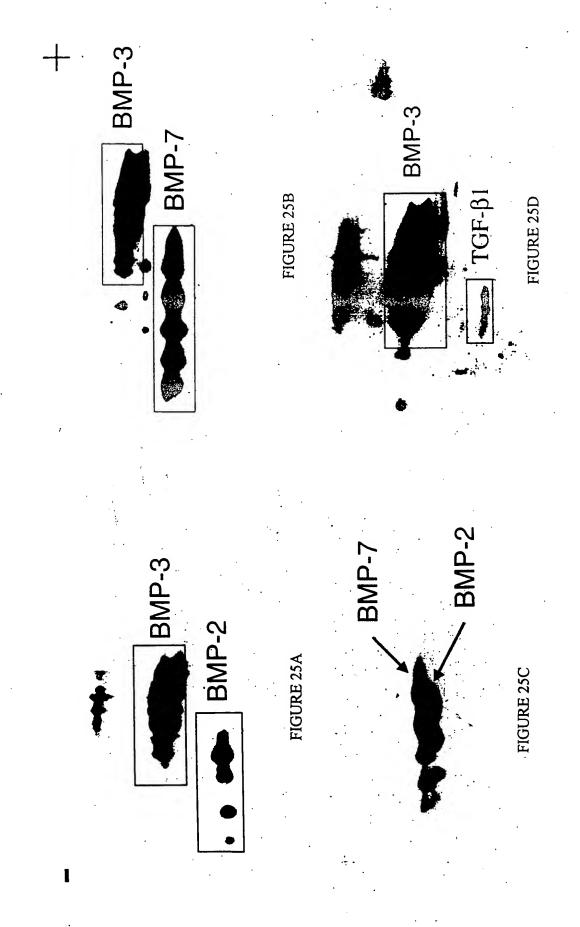
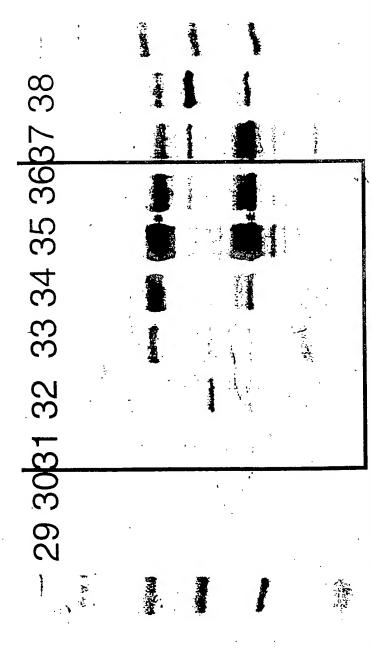
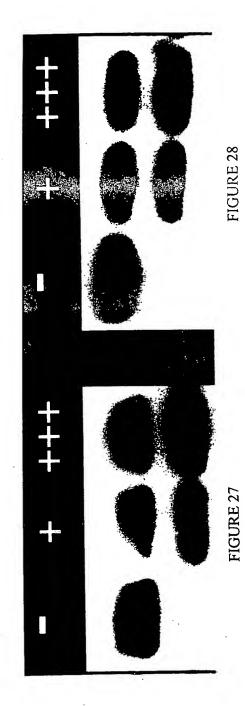


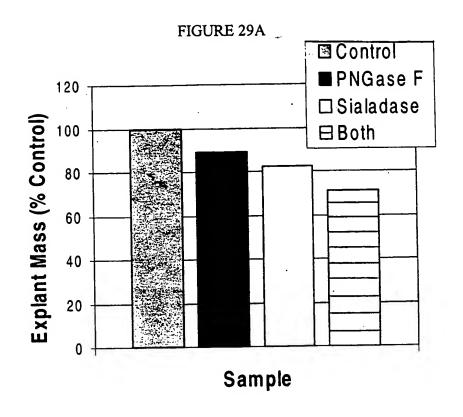
FIGURE 24

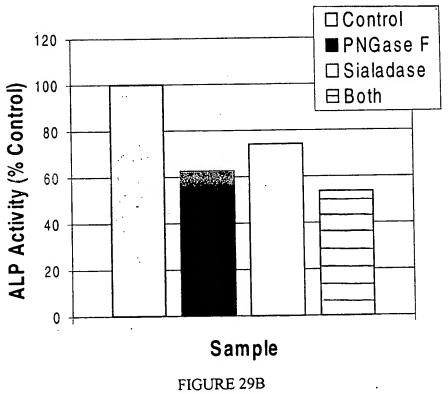


Ø .









.) FIGURE 30

Antibody Information

Specificity	Antigen	Host Species	PC/MC	Source	Catalog No.
TGF-β1 (human)	Protein	Rabbit	Polycional	Promega	G1221
TGF-β2 (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-90
TGF-β3 (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-82
BMP-2 (human)	Protein	Rabbit	Polyclonal	Austral Biologics	PA-513-9
BMP-3 (human)	Peptide	Chicken	Polycional	Research Genetics	NA
BMP-4 (human)	Peptide	Goat	Polycional	Santa Cruz Biotechnology	sc-6896
BMP-5 (human)	Peptide	Goat	Polycional	Santa Cruz Biotechnology	sc-7405
BMP-6 (human)	Peptide	Mouse	Monoclonal	Novocastra Laboratories	NCL-BMP6
BMP-7 (human)	Peptide	Rabbit	Polyclonal	Research Genetics	NA
FGF-1 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-1884
osteonectin (bovine)	Protein	Mouse	Monoclonal	DSHB	AON-1
osteocalcin (bovine)	Protein	Rabbit	Polyclonal	Accurate Chemicals	A761/R1H ·
serum albumin (bovine)	Protein	Rabbit	Polyclonal	Chemicon International	AB870
transferrin (human)	Protein	Chicken	Polycional	Chemicon International	AB797
apo-A1 lipoprotein (human)	Protein	Goat	Polycional	Chemicon International	AB740

Figure 31A. Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments

Band Sample Sequen	Sequen	Sequence Data	Best Database Match Match	$\overline{}$	Identification	Species	Acc. No.	AAs
fx 49 XI AAAGYDVEK AI		Ā	AL AAAGYDVEK	11/11	histone H1.c	human	87668 (NCBI)	65-75
fx 67 SLEKVCADLIR SLEK (1346)		SLEK	SLEKVCADLIR	11/11	40s Ribosomal Protein S20	rat	(<u>위</u>	31-41
fx 65 () (V)VCGMLGFPSEAPV VVCC		OVV	VVCGMLGFPGEKRV	11/14	LORP	mouse	AAC95338 (NCBI)	213- 226
N terminal STGVLLPLQNNELPG STGV seq	PG	STGV	STGVLLPLQNNELPG	15/15	BMP-3	human	4557371 (NCBI)	290- 304
fx 72 STGVLLPLQNNELPGA STGVLI (3925) EYQY AEYQY	LPLQNNELPGA	STGV AEYQ	STGVLLPLQNNELPG 20/20 AEYQY	20/20	BMP-3	human		290- 309
fx 74 STGVLLPLQ STGV (3409)		STGV	STGVLLPLQ	6/6	BMP-3	human		290- 298
fx 55 (S)QTLQFXE SQTLQFDE (1566)		SQTLO		8//	BMP-3	human	4557371 (NCBI)	346- 353
fx 47 VYAF no match		no mat	ch		222			
minal HAGKYSREKNT(P)A(P)		н с ску	HGGKYSREKNQPKP	11/14	α2-Macroglobulin Receptor Assoc. Pro.	human	P30533 (Swiss-Prot)	31-46
7 SQTLQFDEQ 8)		SQTL	SATLAFDEA	6/6	BMP-3	human	4557371 (NCBI)	346- 354
fx 57 SLKPSNHA SLKPSNHA (1652)		SLKP	SNHA	8/8	BMP-3	human	4557371 (NCBI)	410-
fx 51 AALRPLVKP AALRF (1093)		AALRF	AALRPLVKP	6/6	60s Ribosomal Protein L32	monse	P17932 (Swiss-Prot)	1-9
fx 37 (no A(H)I(Q)VERYV AIVER MS)		AIVER		5/5	60s Ribosomal Protein L32	monse	P17932 (Swiss-Prot)	109- 113
fx 37 (no A(H)I(Q)VERYV HQSDRYV MS)		наѕр	RYV	5/7	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	22-28
fx 78 () XALF(G)AQLGXALGPI no match	LGPI	no m	atch	•	555			
SQTLQFDEQT		SQT	SATLAFDEAT	10/10	BMP-3	human	P12645 (Swiss-Prot)	346- 355

Figure 318. Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments

Para	Dand Cample	Sociones Data	Bost Database Match Match	_	Identification	Species	Acc. No.	AAs
Daild	Sample		DCSI Dallabase march			himan	4557371	346-
_	(1311)	מעוראן		0/0			(NCBI)	351
	27.7	NI ATVIVENDY	NI ATVIKBVGGDK	13/13	60s Ribosomal Protein I 6 Ihuman	himan	002878	87-99
	(1772)						(Swiss-Prot)	
	fx 76	XVFAL	VFAL	4/4	60s Ribosomal Protein L6	human	Q02878	273-
	(1795)						(Swiss-Prot)	276
	fx 61	AVPQLQGYLR	AIPalagylr	9/10	60s Ribosomal Protein L6	human	Q02878	262-
	(1145)						(Swiss-Prot)	271
18								
22	fx 58	AI DAAYCFR	ALDAAYCFR	6/6	TGF-82	human	P08112	303-
!	(1101)						(Swiss-Prot)	311
	fx 69 (no	GYNANFCAGACPYL	GYNANFCAGACPYL 14/14	14/14	TGF-82	human	P08112	340-
	match)						(Swiss-Prot)	353
	fx 66	VNSOSLSPY	VNSQSLSPY	6/6	SPP24	bovine	Q27967	42-50
	(1411.71)						(Swiss-Prot)	
25	fx 39	KAAKPSV(P)	KAAKPSVP	8/8	Histone H1.x	human	JC4928 (PIR)	199-
	(1470)							206
29								

fx = fraction number (molecular weight of fragment, as measured by SDS-PAGE)

Figure 32A. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

												_,						
Comments		15 MS peaks match with Band 2				identification of starred peptide confirmed by sequence analysis		15 MS peaks match with Band 1								12 MS peaks match with Band 8		
% Cover-	age	22				16			62							ω		
AAs		110-121	62-79	64-79	35-54	65-79*	64-79	35-54	50-59	76-83	56-66	88-99	9-21	5-21	88-119	150-167	648-669	455-478
Mass Diff-	erence	09.0	0.16	0.58	-0.74	0.05	0.13	-0.20	0.36	-0.09	-0.16	0.55	0.27	-0.17	-0.85	-0.32	-0.28	0.47
Mass	Spec Database	1172.37	1579.71	1707.89	2012.32	1579.71	1707.89	2012.32	1129.40	1156.30	1334.62	1351.58	1517.77	1919.19	3404.87	1988.27	2410.63	2610.10
Mass	Spec Data	1172.97	1579.87	1708.47	2011.58	1579.76	1708.02	2012.12	1129.76	1156.21	1334.46	1352.13	1518.04	1919.02	3404.02	1987.95	2410.35	2610.57
Acc. No.		87668 (NCBI)				87668 (NCBI)			R3RT20 (PIR)							NP002309 (Swiss- Prot)		·
Species		human				human			rat							human		
Mass Spec	Profile	4 peaks match with histone H1.c				3 peaks match with histone H1.c			7 peaks match with ribosome S20							3 peaks match with Lysyl		
Band		-				2			က							4		

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Figure 32B. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

Comments		% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)						identification of starred peptide confirmed by	sequence analysis			-			% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)		
% Cover-	age	48									17				15		
AAs		361-368	346-357	345-357	410-424	346-360	374-392	373-392		290-318*	283-290		129-150	257-282	346-357	410-424	
Mass Diff-	erence	0.01	-0.05	00.00	-0.05	0.07	-0.17	-0.36		1.38	60.0		0.15	-0.01	0.18	-0.03	
Mass	Spec Database	1113.31	1438.58	1566.76	1651.91	1794.02	2268.63	2424.81		3407.77	1002.15		2362.43	3048.52	1566.75	1651.91	
Mass	Spec Data	1113.32	1438.53	1566.76	1651.86	1794.09	2268.46	2424.45		3409.15	1002.24		2362.58	3048.51	1566.93	1651.88	
Acc. No.		4557371 (NCBI)									P30533 (Swiss-	LIOI			4557371 (NCBI)		
Species		human									human				human		
Mass Spec	Profile	9 peaks match with BMP-3									3 peaks match with	αζ- Macroglobuli n RAP			2 peaks match with BMP-3		
Band		5									9						

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Figure 32 C. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

Comments					% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)					12 MS peaks match with Band 4	% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)					
% Cover- age	. 33				21					က	36					
AAs	67-75	1-10*	65-74	19-29	102-111	361-368	190-200	410-424	346-360	648-669	361-368	346-357	345-357	410-424	41-66	290-318
Mass Diff- erence	0.08	60.0-	0.44	0.12	0.22	0.08	-0.32	0.37	-0.40	-0.26	-0.17	0.02	0.01	0:30	0.48	1.17
Mass Spec Database	1033.17	1093.40	1134.28	1449.66	1060.20	1113.31	1360.58	1621.91	1794.02	2410.63	1113.31	1438.58	1566.76	1651.61	2901.19	3407.77
Mass Spec Data	1033.25	1093.31	1134.72	1449.78	1060.42	1113.39	1360.26	1652.28	1793.62	2410.37	1113.14	1438.60	1566.77	1651.91	2901.67	3408.94
Acc. No.	P17932 (Swiss- Prot)				4557371 (NCBI)					NP002309 (Swiss- Prot)	4557371 (NCBI)					
Species	mouse				human					human	human					
Mass Spec Profile	4 peaks match with ribosome L32				5 peaks match with BMP-3					1 peak matches with Lysyl Oxidase RP	6 peaks match with BMP-3					
Band	7									ω	တ					

Figure 32 D. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

																_					_
Comments		% coverage calculation is relative to the mature BMP-	5, 165 AAS (250-42)																		
% Cover-	age	48					16						52				30				
AAs		361-368	410-424	346-360	373-392	290-318	114-122	141-155	10-20		262-271	260-271	303-311	400-409	312-328	340-362	42-53	113-124	86-98	62-77	33-53
Mass Diff-	erence	-0.08	-0.18	-0.44	-0.57	0.57	0.15	0.02	0.03		0.01	90.0	-0.06	-0.16	-0.23	-0.21	-0.67	-0.06	0.04	0.05	-0.10
Mass	Spec Database	1113.31	1651.91	1794.02	2424.81	3407.77	1140.23	1526.86	1059.12		1145.35	1386.68	1101.26	1175.42	2240.60	2691.91	1411.60	1447.65	1540.60	1869.05	2268.57
Mass	Spec Data	1113.23	1651 73	1793.58	2424.24	3408.34	1140.38	1526.88	1059.15		1145.36	1386.74	1101.20	1175.26	2240.37	2691.70	1410.93	1447.59	1540.64	1869.10	2268.47
Acc. No.		4557371 (NCBI)					Q02878 (Swiss- Prot)		P47911	Prot)			P08112 (Swiss- Prot)	(2) -			Q27967 (Swiss- Prot)	•			
Species		human					human		mouse				human		_		bovine				
Mass Spec	Profile	5 peaks match with	5-4MB				5 peaks match with ribosome L6						4 peaks match with	2d-			5 peaks match with SPP24				
Band		11											18								

Figure 32 E. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

				;							25	•								22			Band
				match with BMP-3	5 peaks			•		match with histone H1.x	5 peaks		SPP24	2 peaks				,	TGF-β2	5 peaks		Profile	Mass Spec
			٠		human						human			bovine						human			Species
				(NCBI)	4557371					(PIR)	JC4928		Prot)	Q27967 (Swiss-		-			Prot)	P08112			Acc. No.
3408.86	1651.80	1566.92	1438.83		1060.43	1732.23	1364.57	1349.85	1221.71		1208.46	1447.40		1411.23	2691.61	2240.25	2084.16	1175.13		1101.15	Data	Spec	Mass
3407.77	1651.91	1566.76	1438.58		1060.20	1732.97	1364.59	1350.52	1222.35		1208.40	1447.65		1411.60	2691.91	2240.60	2084.42	1175.42		1101.26	Database	Spec	Mass
1.09	-0.11	0.16	0.25		0.23	-0.74	-0.02	-0.67	-0.64		0.06	-0.25		-0.37	-0.30	-0.35	-0.26	-0.29		-0.11		erence	-Mass Diff-
290-318	410-424	345-357	346-357		102-111	43-57	48-58	107-119	107-118		48-57	113-124		42-53	340-362	312-328	312-347	400-409		303-311			AAs
					31						14			<u>-1</u>						6 3		age	% Cover-
				relative to the mature BMP- 3, 183 AAS (290-472)	% coverage calculation is																		Comments

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Figure 32F. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

			m	ma	29 4		T)	Band Ma
			BMP-3	match with	4 peaks		Profile	Mass Spec
					human			Species
				(NCBI)	4557371			Acc. No.
3409.04	1566.86	1438.70			1113.22	Data	Spec	Mass
3409.04 3407.77	1566.75	1438.58			1113.31	Database	Spec	Mass
1.27	0.11	0.12		٠	-0.09		erence	Mass Diff-
290-318	345-357	346-357			361-368			AAs
					27		age	% Cover-
			3, 183 AAS (290-472)	relative to the mature BMP-	% coverage calculation is			Comments

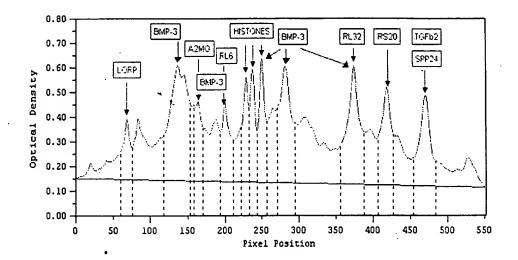


FIGURE 33A

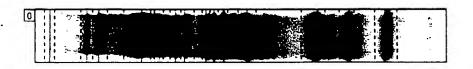


FIGURE 33B

Figure 34. Quantitation of Identified BP proteins

Identified Protein	Percentage of Total Protein
LORP	2
BMP-3	11
BMPO3 & A2-MG	3
RL6 & BMP-3	4
Histone	3
Histone	3
Histone & BMP-3	4
BMP-3	8
RL32 & BMP-3	8
RS20	5
SPP24 & TGF-β2	6
Total	58%